

Exhibit D**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
x_dropoff: **50** expect: **10.0000** wordsize: **3** Filter ☒ View option **Standard**
Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: lcl|seq_1

Length = 14

Sequence 2: lcl|seq_2

Length = 31

No significant similarity was found

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda	K	H
0.334	0.138	0.589

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 7

Number of extensions: 4

Number of sequences better than 10.0: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 14

Length of database: 1,129,354,045

Length adjustment: 0

Effective length of query: 14

Effective length of database: 1,129,354,045

Effective search space: 15810956630

Effective search space used: 15810956630

Neighboring words threshold: 9

X1: 15 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 39 (21.7 bits)

S2: 68 (30.8 bits)